STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____ 10/553,906A _____

Source: _____ IFWO _____

Date Processed by STIC: _____ 11/08/2006 _____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio **(<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/553,906A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 _____ Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

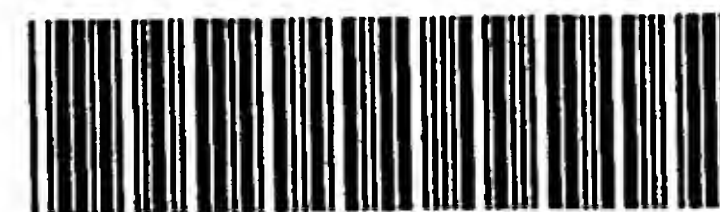9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n or Xaa**, and which residue **n or Xaa** represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 _____ Use of <220>

~~Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.~~ Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa

"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/553,906A

DATE: 11/08/2006
TIME: 13:21:22

Input Set : N:\Crf4\11082006\J533906A.raw
Output Set: N:\CRF4\11082006\J553906A.raw

[handwritten: Invalid]

```
    1 <110> APPLICANT: Skanemejerier AB
    2 <120> TITLE OF INVENTION: NEW ENZYME AND ITS USE
    3 <130> FILE REFERENCE: 75086
C-->  4 <140> CURRENT APPLICATION NUMBER: US/10/553,906A
    5 <141> CURRENT FILING DATE: 2006-03-30
    6 <150> PRIOR APPLICATION NUMBER: US 60/320,139
    7 <151> PRIOR FILING DATE: 2003-04-24
    8 <150> PRIOR APPLICATION NUMBER: US 60/481,598
    9 <151> PRIOR FILING DATE: 2003-11-05
   10 <160> NUMBER OF SEQ ID NOS: 18
   11 <170> SOFTWARE: PatentIn version 3.2
```

[handwritten annotations: On 10/21/05 specification was Amended to the title below → Human Alkaline Sphingomyelinase and use of thereof (Pls correct the title) Does Not Comply Corrected Diskette Needed CPR 1-5]

ERRORED SEQUENCES

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   79 <210> SEQ ID NO: 2
   80 <211> LENGTH: 1701
   81 <212> TYPE: DNA
   82 <213> ORGANISM: Unknown
   83 <220> FEATURE:
   84 <223> OTHER INFORMATION: Unknown
   85 <400> SEQUENCE: 2
```

[handwritten annotations: Ij 22137 Responses are Artificial or Unknown, pls Explains the Source of genetic mater See Item 11 on Error Summary Sheet]

```
E-->  86   gtccatctgg aaggcccagc atgagaggcc cggccgtcct cctcactgtg gctctggcca 60
   87    60
E-->  88   cgctcctggc tcccgggggcc ggagcaccgg tacaaagtca gggctcccag aacaagctgc 120
   89   120
E-->  90   tcctggtgtc cttcgacggc ttccgctgga actacgacca ggacgtggac accccccaacc 180
   91   180
E-->  92   tggacgccat ggccccgagac ggggtgaagg cacgctacat gaccccccgcc tttgtcacca 240
   93   240
E-->  94   tgaccagccc ctgccacttc accctggtca ccggcaaata tatcgagaac cacggggtgg 300
   95   300
E-->  96   ttcacaacat gtactacaac accaccagca aggtgaagct gccctaccac gccacgctgg 360
   97   360
E-->  98   gcatccagag gtggtgggac aacggcagcg tgcccatctg gatcacagcc cagaggcagg 420
   99   420
E--> 100   gcctgagggc tggctccttc ttctacccgg gcgggaacgt cacctaccaa ggggtggctg 480
  101   480
E--> 102   tgacgcggag ccggaaagaa ggcatcgcac acaactacaa aaatgagacg gagtggagag 540
  103   540
E--> 104   cgaacatcga cacagtgatg gcgtggttca cagaggagga cctggatctg gtcacactct 600
  105   600
E--> 106   acttcgggga gccggactcc acgggccaca ggtacggccc cgagtccccg gagaggaggg
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/553,906A

DATE: 11/08/2006
TIME: 13:21:22

Input Set : N:\Crf4\11082006\J533906A.raw
Output Set: N:\CRF4\11082006\J553906A.raw

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E--> 108     agatggtgcg gcaggtggac cggaccgtgg gctacctccg ggagagcatc gcgcgcaacc    720
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E--> 110     acctcacaga ccgcctcaac ctgatcatca catccgacca cggcatgacg accgtggaca    780
       111     780
E--> 112     aacgggctgg cgacctggtt gaattccaca agttccccaa cttcaccttc cgggacatcg    840
       113     840
E--> 114     actttgagct cctggactac ggaccaaacg ggatgctgct ccctaaagaa gggaggctgg    900
       115     900
E--> 116     agaaggtgta cgatgccctc aaggacgccc accccaagct ccacgtctac aagaaggagg    960
       117     960
E--> 118     cgtccccga ggccttccac tacgccaaca accccagggt cacacccctg ctgatgtaca   1020
       119     1020
E--> 120     gcgaccttgg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg   1080
       121     1080
E--> 122     gctttgacaa caaggacatg gacatgaaga ccatcttccg cgctgtgggc cctagcttca   1140
       123     1140
E--> 124     gggcgggcct ggaggtggag ccctttgaga gcgtccacgt gtacgagctc atgtgccggc   1200
       125     1200
E--> 126     tgctgggcat cgtgcccgag gccaacgatg ggcacctagc tactctgctg cccatgctgc   1260
       127     1260
E--> 128     acacagaatc tgctcttccg cctgatgctc tgctggtcgc ggacggaccc tgcctccacca   1320
       129     1320
E--> 130     gcttatccca ggccagaggc tgcatgccac tgtccccggc agcgccaacc cctgcttggc
       131     1380
E--> 132     tgttatggtg ctggtaataa gcctgcagcc caggtccaaa gcccccggcg agccggtccc
       133     1440
E--> 134     ataaccggcc ccctgcccct gccctgctc ctgctcctcc ccttcgggcc ccctcctcct
       135     1500
E--> 136     gcaaaacccg ctcccgaagc ggcgctgccg tctgcagcca cgcgggggcg cgcgggagtc
       137     1560
E--> 138     ttctgcgggc gctggaacct gcagacccgg cctcggtcag ctgggagggg cccgccccgg
       139     1620
E--> 140     cacaaagcac ccatgggaat aaaggccaag ccgcgacagt cagcaaaaaa aaaaaaaaaa
       141     1680
E--> 142     aaaaaaaaaa aaaaaaaaaa a
       143     1701
       222     <210> SEQ ID NO: 5
       223     <211> LENGTH: 1878
       224     <212> TYPE: DNA
       225     <213> ORGANISM: Unknown
       226     <220> FEATURE:
       227     <223> OTHER INFORMATION: Unknown
       228     <220> FEATURE:
       229     <221> NAME/KEY: misc_feature
       230     <222> LOCATION: (905)..(905)
       231     <223> OTHER INFORMATION: n is a, c, g, or t
       232     <400> SEQUENCE: 5
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```

```
      234      60
E--> 235      cgctcctggc tcccggggcc ggagcaccgg tacaaagtca gggctcccag aacaagctgc
     236      120
E--> 237      tcctggtgtc cttcgacggc ttccgctgga actacgacca ggacgtggac accccccaacc
     238      180
E--> 239      tggacgccat ggcccgagac ggggtgaagg cacgctacat gaccccccgcc tttgtcacca
     240      240
E--> 241      tgaccagccc ctgccacttc accctggtca ccggcaaata tatcgagaac cacggggtgg
     242      300
E--> 243      ttcacaacat gtactacaac accaccagca aggtgaagct gccctaccac gccacgctgg
     244      360
E--> 245      gcatccagag gtggtgggac aacggcagcg tgcccatctg gatcacagcc cagaggcagg
     246      420
E--> 247      gcctgagggc tggctccttc ttctacccgg gcgggaacgt cacctaccaa ggggtggctg
     248      480
E--> 249      tgacgcggag ccggaaagaa ggcatcgcac acaactacaa aaatgagacg gagtggagag
     250      540
E--> 251      cgaacatcga cacagtgatg gcgtggttca cagaggagga cctggatctg gtcacactct
     252      600
E--> 253      acttcgggga gccggactcc acgggccaca ggtacggccc cgagtccccg gagaggaggg
     254      660
E--> 255      agatggtgcg gcaggtggac cggaccgtgg gctacctccg ggagagcatc gcgcgcaacc
     256      720
E--> 257      acctcacaga ccgcctcaac ctgatcatca catccgacca cggcatgacg accgtggaca
     258      780
E--> 259      aacgggctgg cgacctggtt gaattccaca agttccccaa cttcaccttc cgggacatcg
     260      840
E--> 261      agtttgagct cctggactac ggaccaaacg ggatgctgct ccctaaagaa gggaggctgg
     262      900
E--> 263      agaangtgta cgatgccctc aaggacgccc accccaagct ccacgtctac aagaaggagg
     264      960
E--> 265      cgttccccga ggccttccac tacgccaaca accccagggt cacaccccctg ctgatgtaca
     266      1020
E--> 267      gcgaccttgg ctacgtcatc catgggagaa ttaacgtcca gttcaacaat ggggagcacg
     268      1080
E--> 269      gctttgacaa caaggacatg gacatgaaga ccatcttccg cgctgtgggc cctagcttca
     270      1140
E--> 271      gggcgggcct ggaggtggag ccctttgaga gcgtccacgt gtacgagctc atgtgccggc
     272      1200
E--> 273      tgctgggcat cgtgcccgag gccaacgatg ggcacctagc tactctgctg cccatgctgc
     274      1260
E--> 275      acacagaatc tgctcttccg cctgatggaa ggcctactct cctgcccaag ggaagatctg
     276      1320
E--> 277      ctctcccgcc cagcagcagg cccctcctcg tgatgggact gctggggacc gtgattcttc
     278      1380
E--> 279      tgtctgaggt cgcataacgc cccatggctc aaggaagccg ccgggagctg cccgcaggcc
     280      1440
E--> 281      ctgggccggc tgtctcgctg cgatgctctg ctggtcgcgg acggaccctg cctccccagc
     282      1500
```

```
E--> 283     ttatcccagg ccagaggctg catgccactg tccccggcag cgccaacccc tgcttggctg      1560
     284     1560

E--> 285     ttatggtgct ggtaataagc ctcgcagccc aggtccagag cccccggcga gccggtccca
     286     1620

E--> 287     taaccggccc cctgcccctg cccctgctcc tgctcctccc cttcgggccc cctcctcctg
     288     1680

E--> 289     caaaacccgc tcccgaagcg gcgctgccgt ctgcagccac gcggggcgc gcgggagctc
     290     1740

E--> 291     tgcgggcgct ggaacctgca gacccggcct cggtcagctg ggaggggccc gccccggcac
     292     1800

E--> 293     aaagcaccca tgggaataaa ggccaagccg cgacagtcag caaaaaaaaa aaaaaaaaaa
     294     1860

E--> 295     aaaaaaaaaa aaaaaaaa
     296     1878

     388 <210> SEQ ID NO: 10
     389 <211> LENGTH: 27
     390 <212> TYPE: DNA
     391 <213> ORGANISM: Unknown
     392 <220> FEATURE:
     393 <223> OTHER INFORMATION: Unknown
     394 <400> SEQUENCE: 10
E--> 395     ggcccagcat gagaggcccg gccgtcc
     396     27

     398 <210> SEQ ID NO: 11
     399 <211> LENGTH: 27
     400 <212> TYPE: DNA
     401 <213> ORGANISM: Unknown
     402 <220> FEATURE:
     403 <223> OTHER INFORMATION: Unknown
     404 <400> SEQUENCE: 11
E--> 405     ggacggccgg gcctctcatg ctgggcc
     406     27

     408 <210> SEQ ID NO: 12
     409 <211> LENGTH: 20
     410 <212> TYPE: DNA
     411 <213> ORGANISM: Unknown
     412 <220> FEATURE:
     413 <223> OTHER INFORMATION: Unknown
     414 <400> SEQUENCE: 12
E--> 415     taatacgact cactataggg
     416     20

     418 <210> SEQ ID NO: 13
     419 <211> LENGTH: 18
     420 <212> TYPE: DNA
     421 <213> ORGANISM: Unknown
     422 <220> FEATURE:
     423 <223> OTHER INFORMATION: Unknown
     424 <400> SEQUENCE: 13
E--> 425     tccgagatct ggacgagc
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RAW SEQUENCE LISTING   DATE: 11/08/2006
PATENT APPLICATION: US/10/553,906A   TIME: 13:21:22

Input Set : N:\Crf4\11082006\J533906A.raw
Output Set: N:\CRF4\11082006\J553906A.raw

```
      426        18
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      430 <212> TYPE: DNA
      431 <213> ORGANISM: Unknown
      432 <220> FEATURE:
      433 <223> OTHER INFORMATION: Unknown
      434 <400> SEQUENCE: 14
E--> 435        ggcccgagac ggggtgaagg cacgctacat gacccccgcc
      436        40
      438 <210> SEQ ID NO: 15
      439 <211> LENGTH: 23
      440 <212> TYPE: DNA
      441 <213> ORGANISM: Unknown
      442 <220> FEATURE:
      443 <223> OTHER INFORMATION: Unknown
      444 <400> SEQUENCE: 15
E--> 445        tggcccgtgg agtccggctc ccc
      446        23
      458 <210> SEQ ID NO: 17
      459 <211> LENGTH: 31
      460 <212> TYPE: DNA
      461 <213> ORGANISM: Unknown
      462 <220> FEATURE:
      463 <223> OTHER INFORMATION: Unknown
      464 <400> SEQUENCE: 17
E--> 465        atggatccat gagaggcccg gccgtcctcc t
      466        31
      468 <210> SEQ ID NO: 18
      469 <211> LENGTH: 31
      470 <212> TYPE: DNA
      471 <213> ORGANISM: Unknown
      472 <220> FEATURE:
      473 <223> OTHER INFORMATION: Unknown
      474 <400> SEQUENCE: 18
E--> 475        acgtcgactt accagcacca taacagccaa g
      476        31
E--> 477        1
```

Same Error (handwritten)

Pls delete (handwritten)

VERIFICATION SUMMARY   DATE: 11/08/2006
PATENT APPLICATION: US/10/553,906A   TIME: 13:21:23

Input Set : N:\Crf4\11082006\J533906A.raw
Output Set: N:\CRF4\11082006\J553906A.raw

```
L:4 M:270 C: Current Application Number differs, Replaced Current Application Number
L:86 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:2
L:88 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:2
L:90 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:180 SEQ:2
L:92 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:240 SEQ:2
L:94 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:2
L:96 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:360 SEQ:2
L:98 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:420 SEQ:2
L:100 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:480 SEQ:2
L:102 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:540 SEQ:2
L:104 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:600 SEQ:2
L:106 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:660 SEQ:2
L:108 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:720 SEQ:2
L:110 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:780 SEQ:2
L:112 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:840 SEQ:2
L:114 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:900 SEQ:2
L:116 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:960 SEQ:2
L:118 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1020 SEQ:2
L:120 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1080 SEQ:2
L:122 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1140 SEQ:2
L:124 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1200 SEQ:2
L:126 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1260 SEQ:2
L:128 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1320 SEQ:2
L:130 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1380 SEQ:2
L:132 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1440 SEQ:2
L:134 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1500 SEQ:2
L:136 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1560 SEQ:2
L:138 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1620 SEQ:2
L:140 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1680 SEQ:2
L:142 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1701 SEQ:2
L:233 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:5
L:235 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:5
L:237 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:180 SEQ:5
L:239 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:240 SEQ:5
L:241 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:5
L:243 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:360 SEQ:5
L:245 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:420 SEQ:5
L:247 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:480 SEQ:5
L:249 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:540 SEQ:5
L:251 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:600 SEQ:5
L:253 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:660 SEQ:5
L:255 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:720 SEQ:5
L:257 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:780 SEQ:5
L:259 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:840 SEQ:5
L:261 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:900 SEQ:5
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:900
L:263 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:960 SEQ:5
L:265 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1020 SEQ:5
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VERIFICATION SUMMARY   DATE: 11/08/2006

PATENT APPLICATION: **US/10/553,906A**   TIME: 13:21:23

Input Set : **N:\Crf4\11082006\J533906A.raw**
Output Set: **N:\CRF4\11082006\J553906A.raw**

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L:269 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1140 SEQ:5
L:271 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1200 SEQ:5
L:273 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1260 SEQ:5
L:275 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1320 SEQ:5
L:277 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1380 SEQ:5
L:279 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1440 SEQ:5
L:281 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1500 SEQ:5
L:283 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1560 SEQ:5
L:285 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1620 SEQ:5
L:287 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1680 SEQ:5
L:289 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1740 SEQ:5
L:291 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1800 SEQ:5
L:293 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1860 SEQ:5
L:295 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1878 SEQ:5
L:395 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:10
L:405 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:11
L:415 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12
L:425 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:13
L:435 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:14
L:445 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:15
L:465 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:17
L:475 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:18
L:477 M:254 E: No. of Bases conflict, this line has no nucleotides.
```